

DPN

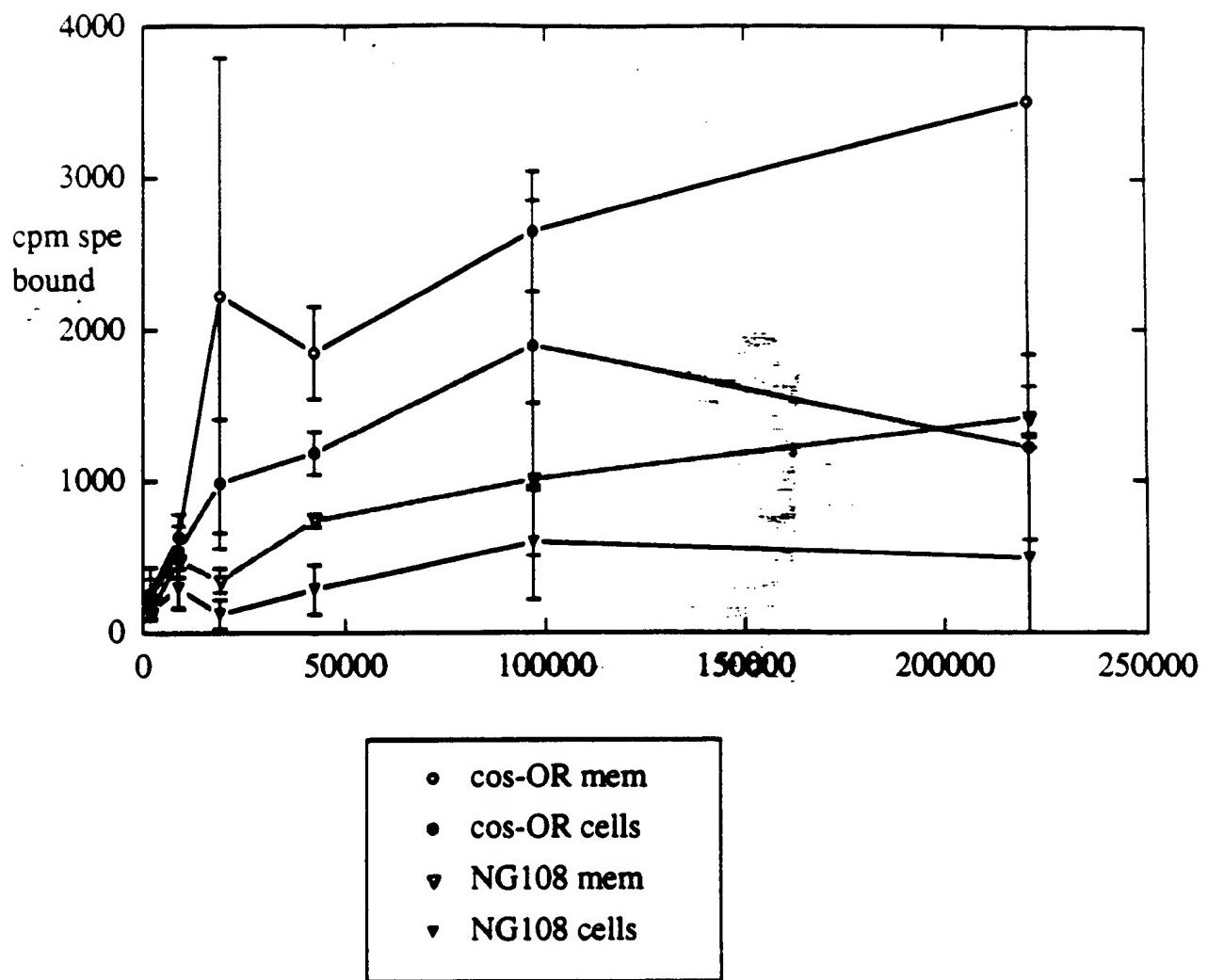


Fig. 1

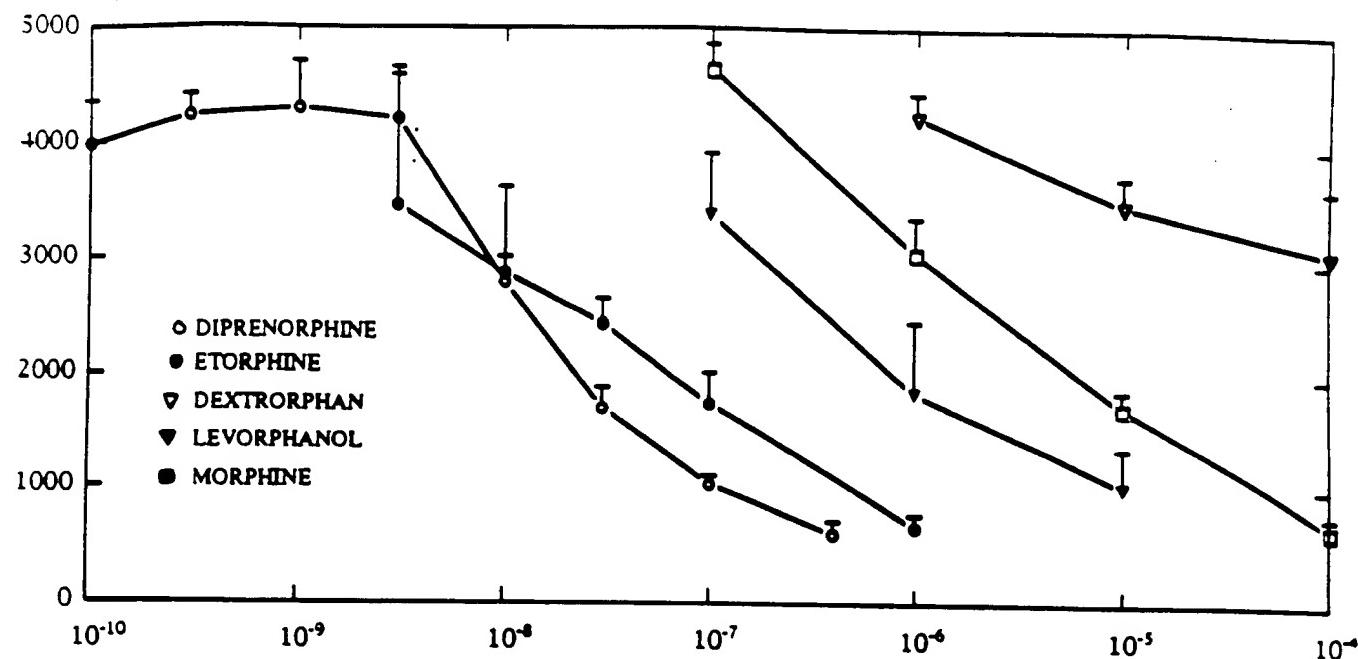


Fig. 2

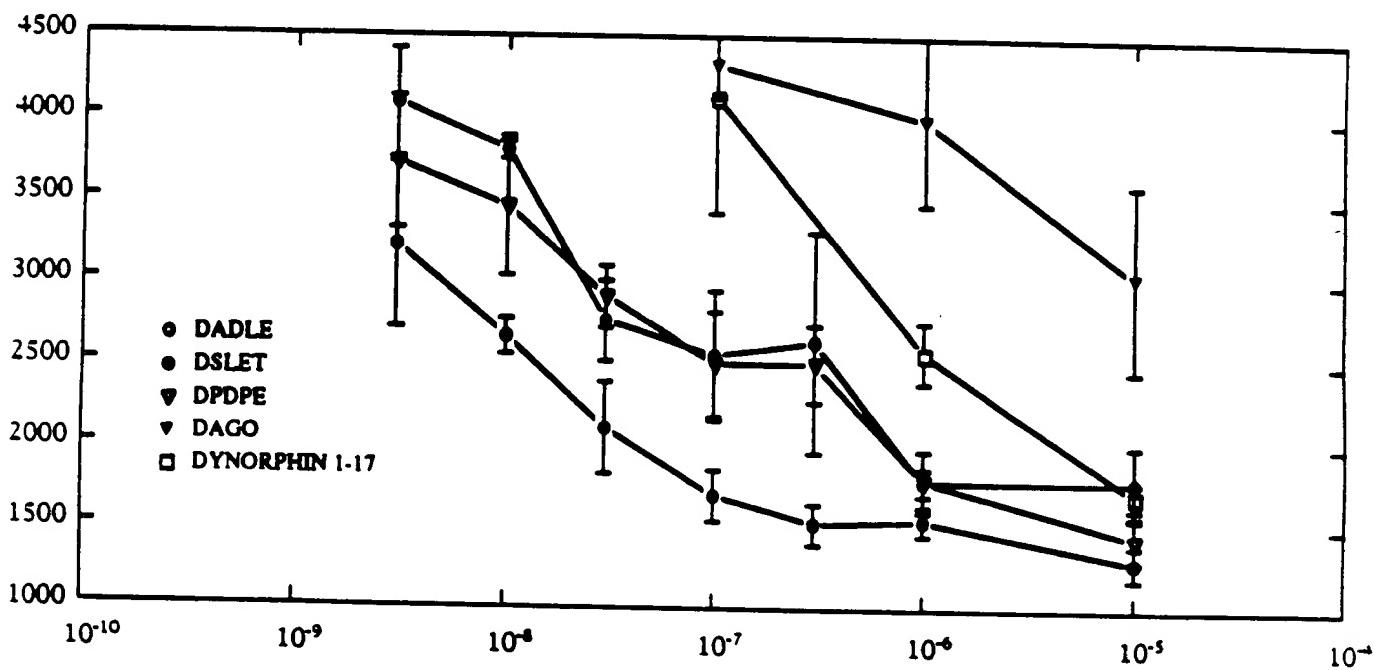


Fig. 3

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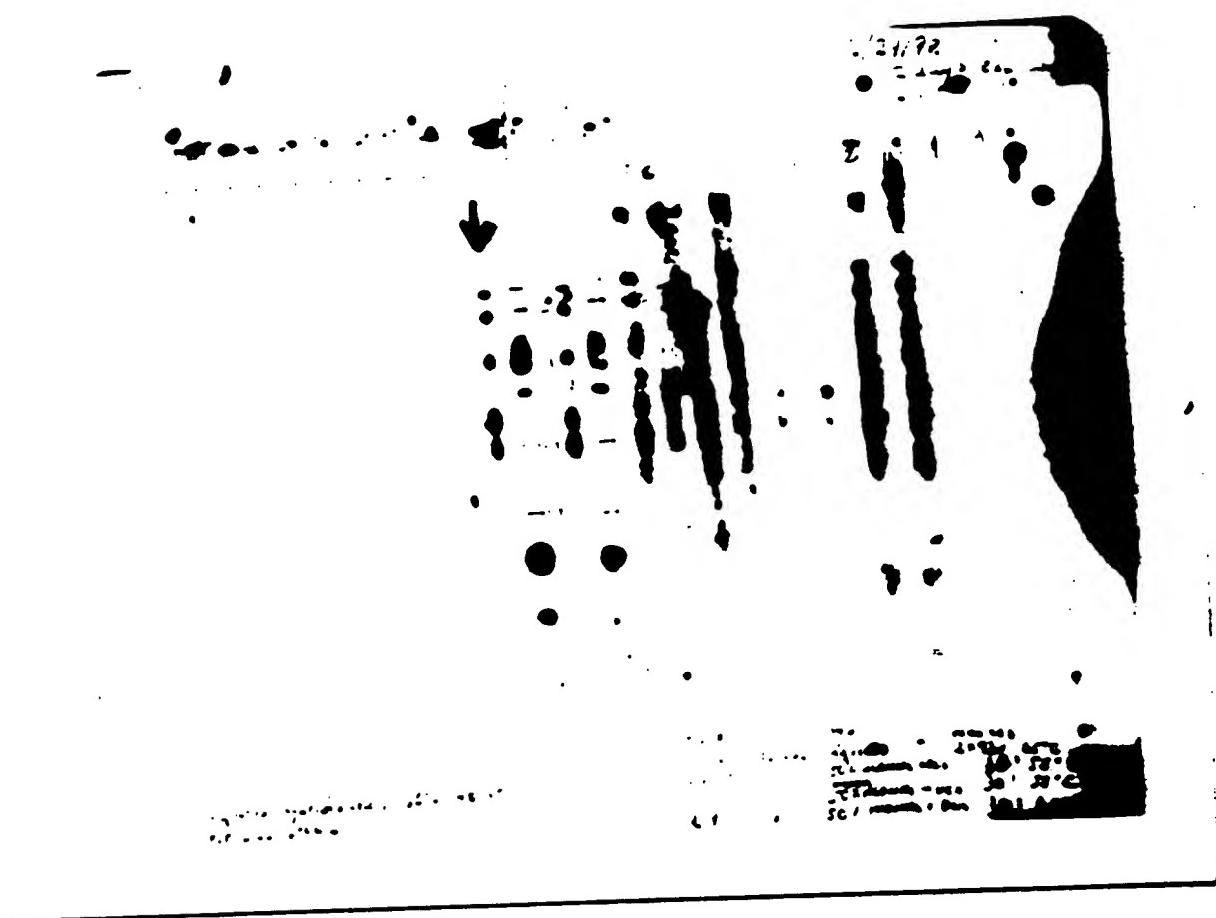


Fig. 4

GCACGGTGGAGACGGACACGGCGGCCATG GAG CTG GTG CCC TCT GCC CGT GCG GAG CTG CAG TCC TCG CCC C
 Met Glu Leu Val Pro Ser Ala Arg Ala Glu Leu Gln Ser Ser Pro L
 GTC AAC CTC TCG GAC GCC TTT CCC AGC GCC TTC CCC AGC GCG GGC GCC AAT GCG TCG GGG TCG CCG G
 Val Asn*Leu Ser Asp Ala Phe Pro Ser Ala Phe Pro Ser Ala Gly Ala Asn*Ala Ser Gly Ser Pro G
 GCC CGT AGT GCC TCG TCC CTC GCC CTA GCC ATC ACC GCG CTC TAC TCG GCT GTG TGC GCA G
 Ala Arg Ser Ala Ser Ser Leu Ala Ala Ile Ala Ile Thr Ala Leu Tyr Ser Ala Val Cys Ala V
 GGG CTT CTG GGC AAC GTG CTC GTC ATG TTT GCC ATC GTC CGG TAC ACC AAA TTG AAG ACC GCC ACC A
Gly Leu Leu Gly Asn Val Leu Val Met Phe Gly Ile Val Arg Tyr Thr Lys Leu Lys Thr Ala Thr A
 ATC TAC ATC TTC AAT CTG GCT TTG GCT GAT GCG CTG GCC ACC AGC ACG CTG CCC TTC CAG AGC GCC A
Ile Tyr Ile Phe Asn Leu Ala Asp Ala Leu Ala Thr Ser Thr Leu Pro Phe Gln Ser Ala L
 TAC TTG ATG GAA ACG TGG CCG TTT GGC GAG CTG CTG TGC AAG GCT GTG CTC TCC ATT GAC TAC TAC A
Tyr Leu Met Glu Thr Trp Pro Phe Gly Glu Leu Leu Cys Lys Ala Val Leu Ser Ile Asp Tyr Tyr Tyr A
 ATG TTC ACT AGC ATC TTC ACC CTC ACC ATG ATG AGC GTG GAC CGC TAC ATT GCT GTC TGC CAT CCT G
Met Phe Thr Ser Ile Phe Thr Met Met Ser Val Asp Arg Tyr Ile Ala Val Cys His Pro V
 AAA GCC CTG GAC TTC CCG ACA CCA GCC AAG GCC AAG CTG ATC AAT ATA TGC ATC TGG GTC TTG GCT T
Lys Ala Leu Asp Phe Arg Thr Pro Ala Lys Leu Ile Asn Ile Cys Ile Tyr Val Val Leu Ala S
 GGT GTC GGG GTC CCC ATC ATG GTC ATG GCA GTG ACC CAA CCC CGG GAT GGT GCA GTG GTA TGC ATG C
Gly Val Gly Val Pro Ile Met Val Val Thr Gln Pro Arg Asp Gly Ala Val Val Cys Met L
 CAG TTC CCC AGT CCC AGC TGG TAC TGG GAC ACT GTG ACC AAG ATC TGC GTG TTC CTC TTT GCC TTC G
Gln Phe Pro Ser Pro Trp Tyr Trp Asp Thr Val Thr Lys Ile Cys Val Phe Leu Phe Ala Phe V
 GTG CCG ATC CTC ATC ACG GTG TGC TAT GGC CTC ATG CTA CTG CGC CTG CGC AGC GTG CGT CTG C
Val Pro Ile Leu Ile Ile Thr Val Cys Tyr Gly Leu Met Leu Leu Arg Leu Arg Ser Val Arg Leu L
 TCC GGT TCC AAG GAG AAG GAC CGC AGC CTG CGG CGC ATC ACG CGC ATG GTG CTG GTG GTG GTG GGC G
Ser Gly Ser Lys Glu Lys Asp Arg Ser Leu Arg Arg Ile Thr Arg Met Val Leu Val Val Val Gly A
 TTC GTG GTG TGC TGG GCG CCC ATC CAC ATC TTC GTC ATC GTC TGG ACG CTG GTG GAC ATC AAT CGG C
Phe Val Val Cys Trp Ala Pro Ile Phe Val Ile Val Trp Thr Leu Val Asp Ile Asn Arg Al
 GAC CCA CTT GTG GTG GCC GCA CTG CAC CTG TGC ATT GCG CTG GGC TAC GCC AAC AGC AGC CTC AAC C
Asp Pro Leu Val Val Ala Ala Leu His Leu Cys Ile Ala Leu Gly Tyr Ala Asn Ser Ser Leu Asn P
 GTT CTC TAC GCC TTC CTG GAC GAG AAC TTC AAG CGC TGC TTC CGC CAG CTC TGT CGC ACG CCC TGC G
Val Leu Tyr Ala Phe Leu Asp Glu Asn Phe Lys Arg Cys Phe Arg Gln Leu Cys Arg Thr Pro Cys G
 CGC CAA GAA CCC GGC AGT CTC CGT CGT CCC CGC CAG GCC ACC ACG CGT GAG CGT GTC ACT GCC TGC A
Arg Gln Glu Pro Gly Ser Leu Arg Arg Pro Arg Gln Ala Thr Thr Arg Glu Arg Val Thr Ala Cys T
 CCC TCC GAC GGC CCG GGC GGT GGC GCT GCC TGA CCTACCCGACCTTCCCCCTAAACGCCCTCCCAAGTGAAGT
Pro Ser Asp Gly Pro Gly Gly Ala Ala Ala ***
 CAGAGGCCACACCGAGCTCCCTGGGAGGTGTGGCCACCACCAAGGACAGCTAGAATTGGGCTTGACAGAGGGAGGCCCTGTGGGG
 GGCTGAGGGATCAAAGGCTCCAGGTTGGAACGGTGGGGTGAGGAAGCAGCAGCTGGTGATTCTAAACTGTATCCATTAGTAAGGCCT
 AATGGGACAGAGCCTCCGCCTTGAGATAAACATCGGTTCTGGCTTTTGAAACACCCAGCTCCAGTCCAAGACCCCAAGGATTCAGCTC
 AACCAAGGGGAGGTGTGATGGGTCGATTTGGTTGGCTGAGAGTCCCAGCATTGTTATGGGGAGGATCTCTCATCTTAGAGA
 AAGGGGACAGGGCATTCAAGGCAAGGCAGCTGGGGTTGGCTAGGAGATAAGGCCCTTCCCTGGGGAGGATAAGTGGGGATG
 ACGTTGGAGAAGAGTCAAAGTCTCACCAACCTTCTAACTACTCAGCTAAACTCGTTGAGGCTAGGGCCAAGTGA
 TACAAGCCGGGCTGTGGGCAAGGCTGTGAAATCCCAGTCATAGTGGAGGCTGAGGCTGGAAAATTAGGACCAACAGCCCCGG

08 / 403260

*20 *40
 MELVPSARAELQSSPLVNLSDAFPSAFPSAGANASGSPGARSAS--SLALAIAITALYSA
: .
 MELTSEQFNGSQWIPSPFDLNGSLGPNGSNQTEPYYDMTSNAVLTFIYFV
 60 80 100
VCAVGILLGNVLVMFGIVRYTKLKTATNIYIENLAADALATSTLPFQSAKYLMETWPFGE
: .
 VCVVGLCGNTLVIVILRYAKMKTITNIYIILNLAIADELFMLGLPFLAMQVALVHWPFGK
 120 140 160
LLCAVLSIDYXNMFTSIFTLIMMSVDYIAVCHPVKALDFRTPAKAKLINICIWVLASG
: .
 AICRVVMTVDGINQFTSIFCLTVMSIDRYLAVVHPIKSAKRRPRTAKMINVAVGVSLL
 180 200 220
VGVPIIMMAVTOPRD-GAVVCMLOQFPSPSWYWDVTVKICVLEFAFVVRILLITVCYGLML
: .
 VILPIMITYAGLRSNQWGRSSCTINWPGESGAWTGFIIYAPILGFLVPLTIICLCYLFII
 240 260 280
LRLRSVRLLSGSKEKDRSLRRITRMVLVVGAFVVCWAPIHIFVTWTLVDINRRDPLVV
: .
 IKVKSSGIRVGSSKRKKSEKKVTRMVSIVAVFIFCWLPFYIPNVSSVVAIS-PTPAALK
 300 320 340
AALHICIALGYANSSLNPVLYAFLDENFKRCFRQ-LCRTPCGRQEPGSLRRPQATTRE
: .
 GMFDPVVILTYANSCANPILYAFLSDNFKKSFQNVLCLVKVSGAEDGERSDSKQDKSRLN
 360 370
 VTACTPSDGPGGGAAA
 ETMHEORTLILNGDLOTSI

Fig. 6.

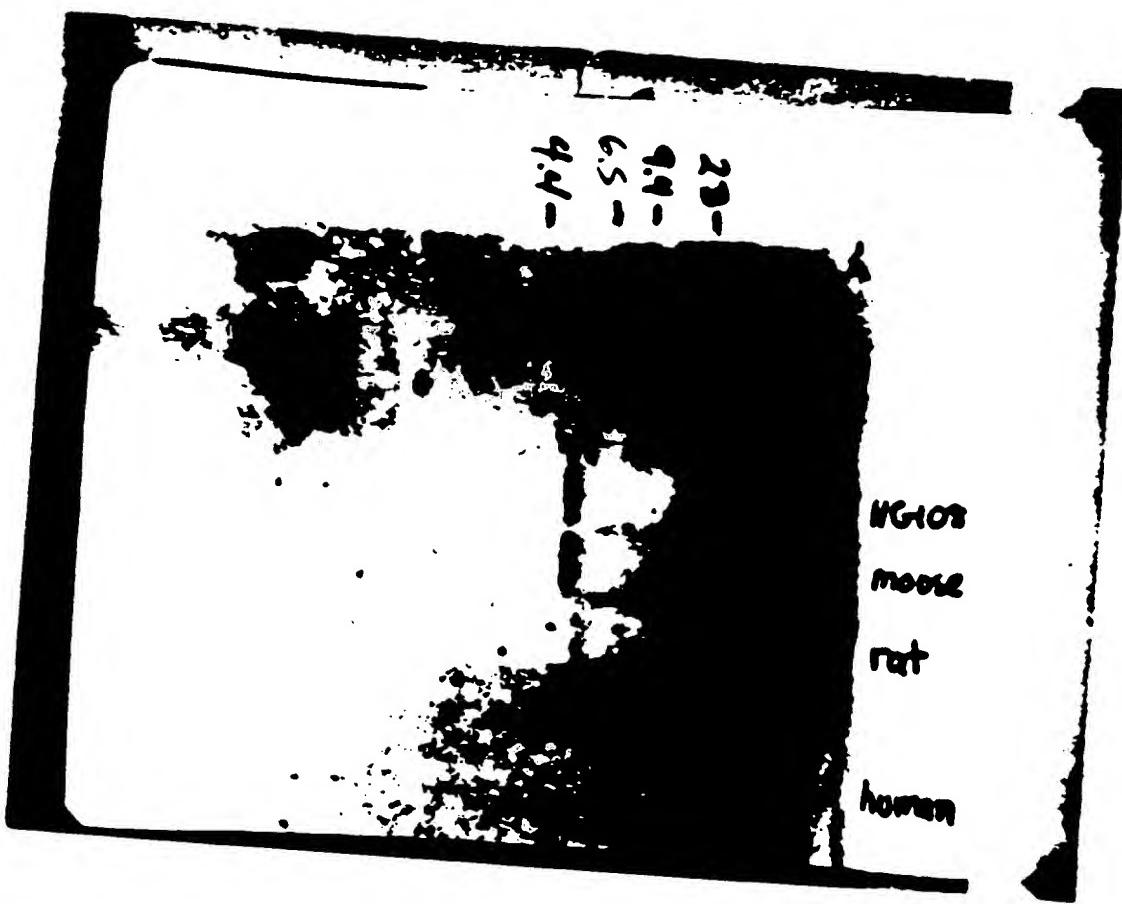


Fig. 7

HUMAN DELTA

Sequence Range: -131 to -1

	-122	-112	-102	-92	-82
Tuyet's H3	-GG GCA GTG GTG TGC ATG CTC CAG TTC CCC AGC CCC AGC TGG TAC TGG GAC ACG				
DOR-1 [478]	610 620 630 640 650 660 gGt GCA GTG GTa TGC ATG CTC CAG TTC CCC AGt CCC AGC TGG TAC TGG GAC ACT> -^v ^^^ ^^^ ^^v ^^^ ^^^ ^^^ ^^^ ^^^ ^^^ ^^v ^^^ ^^^ ^^^ ^^^ ^^^ ^^^ ^^v ^^^ ^^^ ^^v				

	-72	-62	-52	-42	-32
Tuyet's H3	GTG ACC AAG ATC TGC GTG TTC CTC TTC GCC TTC GTG GTG CCC ATC CTC ATC ATC				
DOR-1 [478]	670 680 690 700 710 GTG ACC AAG ATC TGC GTG TTC CTC TTT GCC TTC GTG GTG CCg ATC CTC ATC ATC> ^^^ ^^^ ^^^ ^^^ ^^^ ^^^ ^^^ ^^^ ^^v ^^^ ^^^ ^^^ ^^^ ^^v ^^^ ^^^ ^^^ ^^v				

	-22	-12	-2
Tuyet's H3	ACC GTG TGC TAT GGC CTC ATG CT		
DOR-1 [478]	720 730 ACg GTG TGC TAT GGC CTC ATG C> ^v ^^^ ^^^ ^^^ ^^^ ^^^ ^^		

08/403260

CCT GCG CTT TTG GGG ATG TGC TGT GCA AGA TAG TAA TTT CCA TTG
 50 60 70 80 90
 ATT ACT ACA ACA TGT TCA CCA GCA TCT TCA CCT TGA CCA TGA TGA
 100 110 120 130
 GCG TGG ACC GCT ACA TTG CCG TGT GCG ACC CCG TGA AGG CTT TGG
 140 150 160 170 180
 ACT TCC GCA CAC CCT TGA AGG CAA AGA TCA TCA ATA TCT GCA TCT
 190 200 210 220
 GGC TGC TGT CGT CAT CTG TTG GCA TCT CTG CAA TAG TCC TTG GAG
 230 240 250 260 270
 GCA CCA AAG TCA GGG AAG GTA AGA GCA GTC ATT TCA TTC TGT TCA
 280 290 300 310
 TAA AAA TGT AGC TTC AAA TTA CAT AGA CTT TTA ATT TGA GCG TGA
 320 330 340 350 360
 GTA GGC CAC ATA TTT GTG GAA ATC GAT GCC AAA AGA CGA CGG AAA
 370 380 390 400
 TGT AGT GCC TAA ATC CAT GGA AGA TGA GAA GTA GAA CAA TTT TTT
 410 420 430 440 450
 GTC CCT TTC CAC CTC TAA ACA CAG AAT GCA ATA ATG ACA TTG CCA
 460 470 480 490
 GAA GAG AGA TGC CCG ACC TGT CTC CCA TTC TGG CAA TGT TTA GTA
 500 510 520 530 540
 GAA AGT GGA GGG GTG AGG ATG AGG TAA GAA CCA CAG GCA TGT AGA
 550 560 570 580
 TTT TAA AGT ACA ACC TGG CAA GTC CAG ACA CAC CTT CTC ACT CCT
 590 600 610 620 630
 TTT TTT CTC TTT AAC AAG GGA TAT AAA TTA TTG GTG ACA TAT GCT
 640 650 660 670
 GGT TGT TTC CTC TTT TAT TCC TAA AGG ATA ACC TCC AAA TCA CTA
 680 690 700 710 720
 TTT TAA CAG CTT TGG CGT AGG ATC TCA AAA TCA AGT TAA CGG ATG

Figure 8b (1)

08/403260

730 740 750 760
GTA GTT ACA GAT GAG TCA GAA CCA CTT GAT TTG AAC ATA TCA CCT
770 780 790 800 810
TTT CCC TTG CAA ACC AGC CAA CTG ATT TTT TTT TTT TTT TTT TTT
820 830 840 850
GAG AGA GAG TCT TGC TCT GTC AGG CTA GAG TGC AGT GGC GCG
860 870 880 890 900
ATA TCG GCT CAC TGC AAC CTC TGC CTC CCG GGT TCA ACC TCA GCC
910 920 930 940
TCT CGA GTA GCT GGG ACT ACT GCC ACA CAC CAC CAT GCC CAG CTA
950 960 970 980 990
ATT TTT GTA TTT TTA GTA GAG ACA GGG TTT CAC CGT GTT GGC CAG
1000 1010 1020 1030
GGT GGT CTC AAT CTC TTG ACC TCG TGA TCT GCC CGC CTC GNC TCC
1040 1050 1060 1070 1080
CCA AAG TGC TGG GAT TAC AGG CGT GCN CTG CNC CCG NCC CCT GTT
1090 1100 1110 1120
GAT GTT TTT CCT GTA TTT CTA GGA CAG TAG TTC TCA CTC TGG GCT
1130 1140 1150 1160 1170
GCA CAT TGG AAT CAC CTG GGT ACT TTA GAA AAC ACT GCT GCC TGC
1180 1190 1200 1210
ATC CCA CCC CTT AAG GGT CTG GTG TAA TTG ACC TGG GGT ACA GCC
1220 1230 1240 1250 1260
TGG GTG TCA AGA TTT TTG AGC TCT CTC CAG GTG ACT CTG ACC TGC
1270 1280 1290 1300
AGC CAA GGT GAG AGG TAC TGT TCT AGG AGT TTT GCT TTA CTA GCA
1310 1320 1330 1340 1350
AAA TAT AAA GCT ATA GAA AGC ATC TTT TGT TCC TCA TAG AAA TTA
1360 1370 1380 1390
ATG ATG GGG AGG TGA GCA GAA TAG TCA CTC TGG GCC TAC TCA TGC
1400 1410 1420 1430 1440

Figure 8b (2)

TGT TTA A CAG CAG GTA TAT AGG TTC TC TAC TAG GGG 08/403260
 1450 1460 1470 1480
 GTT CAT AAT ACC TGT GAG AGC AGA TAA CTG AGT GTA TAT AGT GAG
 1490 1500 1510 1520 1530
 GAT TTC CAG GTC ATA GTG AAA GGG CAA GCC ACT AAA ATC ATA GCT
 1540 1550 1560 1570
 TGT CTT GCA TAT ACT GTT TGT TTG TTT TTA GAC TTA CAT GTT AGG
 1580 1590 1600 1610 1620
 TTT CAG TTT ACG TTT TAG GTT CAC AGC AAA ACT GAC CAG AAA GCA
 1630 1640 1650 1660
 CAG AGA GGC ACT TCA ATT TAC CTC CAT TTA CCC CAC ACA GGC ACA
 1670 1680 1690 1700 1710
 TCC TCC CCT ACA GAG TGG TCC ATT TAT TAC AGC TGC TGA ACC CAC
 1720 1730 1740 1750
 ACT GAC ACG CTG TTA TCA CTC AGA GCC TGG CAG TTT ACA GAG GCT
 1760 1770 1780 1790 1800
 CAC TCT CCG NTA TGT GTC CTG TGN TTT GAA CAA ATG TAT AAT GAC
 1810 1820 1830 1840
 TTT ATT CAT TGT TTT TTA ATG AAG CTG ATC TTT TCC CTC TGA AAC
 1850 1860 1870 1880 1890
 TAC AAA ATG AAT TTC TAG CAT AGC CAT AGC AGG TGT CAA GCT ATA
 1900 1910 1920 1930
 CTA CTA GGT AAA TTT TAA GAA ATG CCC AAC TTT ATC ATA TTT GCA
 1940 1950 1960 1970 1980
 TTT CAA AAT ATG ATT AAT CAC ACA TAG GAT TTT GTT TCT TCA TGC
 1990 2000 2010 2020
 CTA CAG CAA ATA GAA ATA AAG TGC AAG AAA CTT TTC TGA GGC AAA
 2030 2040 2050 2060 2070
 GCT TTC ACT TTG TGA ACG TAA AAT GTT GAC TCT AAT ATT TTC CAT
 2080 2090 2100 2110
 ACT GTA GTA TAT GTG TGT GTA TTA TGT GAG GAT TCA TAG TCT GCT
 2120 2130 2140 2150 2160

Figure 8b (3)

08/403260

CTT ACT TTT TTA TAG TAG CTA AGA ATT ATT ATA ATC GCT ATA AGC
2170 2180 2190 2200
AGA AAC AAT TAT TCT TAA CAA AAT GAA TAC ACA CAA GAA AAG CTT
2210 2220 2230 2240 2250
TAG TTT AGC TAT TAG AAC TAA CTC TAT AAT TAT GAT AAC CAT GAG
2260 2270 2280 2290
ATG CTG GAA CAG GAG CCA GCA GAA GCC ACA GCC CTC TGA TAT TAA
2300 2310 2320 2330 2340
TAT ATA AAG AAA CCA AAA TCT GCT TGT TAA ACT GAG GCA GTT GTA
2350 2360 2370 2380
TGG ATA CTT CAA CCT GAA AAT GCC CCC TTC TTC CTG AAA CAG AAC
2390 2400 2410 2420 2430
ATT TAA TAA AAA TGG CAT GCT TGG ACA GGA ATT TCT TTT TTA AAA
2440
AAT GCT TAG TTT TTA TG

Best Available Copy

40

~~~~TTT TAT CTC CTA GAT ACA CCA A~~~~GA CTG CCA CC~~~~**403260**

50 60 70 80 90

TCT ACA TTT TCA ACC TTG CTC TGC AGA TGC CTT AGC CAC CAG TAC

100 110 120 130

CCT GCC CTT CCA GAG TGT GAA TTA CCT AAT GGG AAC ATG GCC ATT

140 150 160 170 180

TGG AAC CAT CCT TTG CAA GAT AGT GAT CTC CAT AGA TTA CTA TAA

190 200 210 220

CAT GTT CAC CAG CAT ATT CAC CCT CTG CAC CAT GAG TGT TGA TCG

230 240 250 260 270

ATA CAT TGC AGT CTG CCA CCC TGT CAA GGC CTT AGA TTT CCG TAC

280 290 300 310

TCC CCN NNN NNN

320 330 340 350 360

NNN NNN

370 380 390 400

NNN NNN NNG TTC CAT AGA TTG TAC ACT AAC ATT CTC TCA TCC AAC

410 420 430 440 450

CTG GTA CTG GGA AAA CCT GCT GAA GAT CTG TGT TTT CAT CTT CGC

460 470 480 490

CTT CAT TAT GCC AGT GCT CAT TAC CGT GTG CTA TGG ACT GAT

500 510 520 530 540

GAT CTT GCG CCT CAA GAG TGT CCG CAT GCT CTC TGG CTC CAA AGA

550 560 570 580

AAA GGA CAG GAA TCT TCG AAG GAT CAC CAG GAT GGT GCT GGT GGT

590 600 610 620 630

GGT GGC TGT GTT CAT CGT CTG CTG GAC TCC CAT TCA CAT TTA CGT

640 650 660 670

CAT CAT TAA AGC CTT GGT TAC AAT CCC AGA AAC TAC GTT CCA GAC

680 690 700 710 720

TGT TTC TTG GCA CTT CTG CAT TGC TCT AGG TTA CAC AAA CAG CTG

730 740 750 760

CCT CAA CCC AGT CCT TTA TGC ATT TCT GGA TGA AAA CTT CCA CGA

770 780 790 800 810

TGC TTC AGA GAG TTC TGT ATC CCA ACC TCT TCC AAC ATT GAG CAA

820 830

CAA AAC TCC ACT CGA ATT CC

Figure 8c

10            20            30            40  
GGG TAC CGG GCC CCC CCT CGA GGT CGA CGG TAT CGA TAA GCT TGA  
50            60            70            80            90  
TAT CGA ATT CTT ACT GAA TTA GGT ATC TTT CTT CAC ACT ACT TGG  
100            110            120            130  
TAA AAA AAA TGA AAA GGC AGA AAA ATT AGC CCC AAA AGA GAT GAA  
140            150            160            170            180  
ACT CTT CCG TCC ATC ACC ATT GAC TCT ATT GTG AAC TTA TGA AAA  
190            200            210            220  
AGG TAG TTG AGC AAT ATG AAG GCC ATG ATG TGG AAT TAA ~~A~~ CA CAC  
230            240            250            260            270  
ACA CAC ACA CAC ACA CAC ACA CAC ~~CAT~~ GCT GGA TTC TAA ATG  
280            290            300            310  
TGT CCT TCC TCC TCT CAC TCT CTT GAT TCA AGT TTA TTT CTG AAC  
320            330  
TGA GAC ACG ATC ACC AC

Figure 8d

10            20            30            40

CGG ATC CTT AGC ATC CCC AAA GCG CCT CCG TGT ACT TCT AAG GTG

50            60            70            80            90

GGA GGG GGA TAC AAG CAG AGG AGA ATA TCG GAC GCT CAG ACG TTC

100            110            120            130

CAT TCT GCC TGC CGC TCT TCT CTG GTT CCA CTA GGG CTT GTC CTT

140            150            160            170            180

GTA AGA AAC TGA CGG AGC CTA GGG CAG CTG TGA GAG GAA GAG GCT

190            200            210            220

GGG GCG CCT GGA ACC CGA ACA CTC TTG AGT GCT CTC AGT TAC AGN

230            240            250            260            270

CTA CCG AGT CCG CAG GAA GCA TTC AGA ACC ATG GAC AGC AGC GCC

280            290            300            310

GGC CCA GGG AAC ATC AGC GAC TGC TCT GAC CCC TTA GCT CCT GCA

320            330            340            350            360

AGT TGC TCC CCA GCA CCT GGC TCC TGG CTC AAC TTG TCC CAC GTT

370            380            390            400

GAT GGA AAC CAG TCC GAC CCA TGC GGT CCT AAC CCG ACG GGC CTT

410            420            430            440            450

GGC GGG AAC GAC AGC CTG TGC CCT CAG ACC GGC AGC CCT TCC ATG

460            470            480            490

GTC ACA GCC ATC ACC ATC ATG GCC CTC TAT TCT ATC GTG TGT GTA

500            510            520            530            540

GTG GGC CTC TTT GGA AAC TTC CTG GTC ATG TAT GTG ATT GTA AGA

550            560            570            580

TAT ACC AAA ATG AAG ACT GCC ACC AAC ATC TAC ATT TTC AAC CTT

590            600            610            620            630

GCT CTG GCA GAT GGC TTA GCC ACT AGC ACG CTG CCC TTT CAG AGT

640            650            660            670

GTT AAC TAC CTG ATG GGA ACG TGG CCC TTT GGA AAC ATC CTC TGC

680            690            700            710            720

AAG ATC GTG ATC TCA ATA GAC TAC TAC AAC ATG TTC ACC AGT ATC

Figure 9 (1)

730                  740                  750                  760  
 TTC ACC CTC TGC ACC ATG AGT GTA GAC CGC TAC ATT GCC GTC TGC  
 770                  780                  790                  800                  810  
 CAC CCG GTC AAG GCC CTG GAT TTC CGT ACC CCC CGA AAT GCC AAA  
 820                  830                  840                  850  
 ATT GTC AAT GTC TGC AAC TGG ATC CTC TCT TCT GCC ATT GGT CTG  
 860                  870                  880                  890                  900  
 CCC GTA ATG TTC ATG GCA ACC ACA AAA TAC AGG CAG GGG TCC ATA  
 910                  920                  930                  940  
 GAT TGC ACC CTC ACG TTC TCT CAT CCC ACA TGG TAC TGG GAG AAC  
 950                  960                  970                  980                  990  
 CTG CTC AAA ATC TGT GTC TTC ATC TTC GCC TTC ATC ATG CCG GGC  
 1000                 1010                 1020                 1030  
 CTC ATC ATC ACT GTG TGT TAT GGA CTG ATG ATC TTA CAG CTC AAG  
 1040                 1050                 1060                 1070                 1080  
 AGT GTC CGC ATG CTG TCG GGC TCC AAA GAA AAG GAC AGG AAC CTG  
 1090                 1100                 1110                 1120  
 CGC AGG ATC ACC CGG ATG GTG CTG GTG GTC GTG GCT GTA TTT ATT  
 1130                 1140                 1150                 1160                 1170  
 GTC TGC TGG ACC CCC ATC CAC ATC TAT GTC ATC ATC AAA GCA CTG  
 1180                 1190                 1200                 1210  
 ATC ACG ATT CCA GAA ACC ACT TTC CAG ACT GTT TCC TGG CAC TTC  
 1220                 1230                 1240                 1250                 1260  
 TGC ATT GCC TTG GGT TAC ACA AAC AGC TGC CTG AAC CCA GTT CTT  
 1270                 1280                 1290                 1300  
 TAT GCG TTC CTG GAT GAA AAC TTC AAA CGA TGT TTT AGA GAG TTC  
 1310                 1320                 1330                 1340                 1350  
 TGC ATC CCA ACT TTC TCC ACA ATC GAA CAG CAA AAC TCT GCT CGA  
 1360                 1370                 1380                 1390  
 ATC CGT CAA AAC ACT AGG GAA CAC CCC TCC ACG GCT AAT ACA GTG  
 1400                 1410                 1420                 1430                 1440

Figure 9 (2)

GAT CGA ACT AAC CAC CAG CTA GAA AAT CTG GAA GCA GAA ACT GCT  
 1450                1460                1470                1480  
 CCA TTG CCC TAA CTG GGT CCC ACG CCA TCC AGA CCC TCG CTA AAC  
 1490                1500                1510                1520                1530  
 TTA GAG GCT GCC ATC TAC TTG GAA TCA GGT TGC TGT CAG GGT TTG  
 1540                1550                1560                1570  
 TGG GAG GCT CTG GTT TCC TGG AAA AGC ATC TGA TCC TGC ATC ATT  
 1580                1590                1600                1610                1620  
 CAA AGT CAT TCC TCT CTG GCT ATT CAC GCT ACA CGT CAG AGA CAC  
 1630                1640                1650                1660  
 TCA GAC TGT GTC AAG CAC TCA GAA GGA AGA GAC TGC AGG CCA CTA  
 1670                1680                1690                1700                1710  
 CTG AAT CCA GCT CAT GTA CAG AAA CAT CCA ATG GAC CAC AAT ACT  
 1720                1730                1740                1750  
 CTG TGG TAT GTG ATT TGT GAT CAA CAT AGA AGG TGA CCC TTC CCT  
 1760                1770                1780                1790                1800  
 ATG TGG AAT TTT TAA TTT CAA GGA AAT ACT TAT GAT CTC ATC AAG  
 1810                1820                1830                1840  
 GGA AAA ATA GAT GTC ACT TGT TAA ATT CAC TGT AGT GAT GCA TAA  
 1850                1860                1870                1880                1890  
 AGG AAA AGC TAC CTC TGA CCT CTA GCC CAG TCA CCC TCT ATG GAA  
 1900                1910                1920                1930  
 AGT TCC ATA GGG AAT ATG TGA GGG AAA ATG TTG CTT CCA AAT TAA  
 1940                1950                1960                1970                1980  
 ATT TTC ACC TTT ATG TTA TAG TCT AGT TAA GAC ATC AGG GGC ATC  
 T

## HIGH HOMOLOGY BETWEEN DELTA, MU AND KAPPA OPIOID RECEPTORS

|       | 10                                                                                                                                                             | 20 | 30 | 40 | 50 |
|-------|----------------------------------------------------------------------------------------------------------------------------------------------------------------|----|----|----|----|
| DOR-1 | MELVPSARAE <u>LQSSPLVNLSDAFFPSAGANASGSPGARSASSLAL</u>                                                                                                          |    |    |    |    |
| rMORa | 10 20 30 40 50 60<br>m <u>dsstgpgntscsdplaqascspapgswinlshvdgNqSDpcginrtglGgNdS1cPqt-gspS</u> <u>mvtA1&gt;</u>                                                 |    |    |    |    |
| rKORa | 10 20 30 40 50 60<br>mespiqifrgdpptcspsacilpnssswfpnwaesdsngsvgsedqqlesahiSpAlpv>                                                                              |    |    |    |    |
|       | 60 70 80 90 100 110 120                                                                                                                                        |    |    |    |    |
| DOR-1 | AITALYSAVCAVGL <u>ENVLUMFGIURYTKLKTATNIYIENLALADALATSTLPFQSAKYL</u> <u>METWPFGELL</u>                                                                          |    |    |    |    |
| rMORa | 70 80 90 100 110 120 130<br><u>u</u> <u>lmALYSivCVvVGLfGNfLV</u> <u>MvvIURYTKmKTATNIYIENLALADALATSTLPFQSVnYLMgTWPFGt</u> <u>l</u> >                            |    |    |    |    |
| rKORa | 70 80 90 100 110 120 130<br><u>u</u> <u>ITAVYVsvfV</u> <u>GVLvGNSLVMFvLi</u> <u>URYTKmKTATNIYIENLALADALyTtTmPFQSAvYLMnsWPFGdvL</u> >                           |    |    |    |    |
|       | 130 140 150 160 170 180 190                                                                                                                                    |    |    |    |    |
| DOR-1 | CKAVL <u>SIDYYNMFTSIETLT</u> <u>MMMSVDRYIAVCPVKALDFRTPAKAKL</u> <u>INICIWVLASGVGVRIMVMAVTQ</u>                                                                 |    |    |    |    |
| rMORa | 140 150 160 170 180 190 200<br><u>CKiVi</u> <u>SIDYYNMFTSIETLc</u> <u>MSVDRYIAVCPVKALDFRTPrnAKi</u> <u>NvCnWiLsSaiG1PvMfMa</u> <u>Tk</u> >                     |    |    |    |    |
| rKORa | 140 150 160 170 180 190 200<br><u>CKiVi</u> <u>SIDYYNMFTSIETLT</u> <u>MMMSVDRYIAVCPVKALDFRTPIKAKi</u> <u>INICIWLLASsVGisaiVlgcTk</u> >                         |    |    |    |    |
|       | 200 210 220 230 240 250 260                                                                                                                                    |    |    |    |    |
| DOR-1 | PRDGAVV <u>CMLQFPSPSWY</u> <u>WDTVTKICVF</u> <u>LFAFVVPI</u> <u>LIIITVCYGLMLRLRSVRLLSGSKEKDRLSLRRIT</u>                                                        |    |    |    |    |
| rMORa | 210 220 230 240 250 260 270<br><u>yRqGsidCtLc</u> <u>FshPtWYWe</u> <u>n11KICVF</u> <u>iFAFimP</u> <u>ILLIITVCYGLMLRLKS</u> <u>SVRnLSGSKEKDRLnLRRIT</u> >       |    |    |    |    |
| rKORa | vd ys<br>  210   230 240 250 260 270<br><u>vRedvieCsLQFPd</u> <u>deW-WD1fmKICVF</u> <u>yFAFViPv</u> <u>LLiVCYtLMi</u> <u>RLKS</u> <u>VRLLSGSrEKDRnLRRIT</u> >  |    |    |    |    |
|       | 270 280 290 300 310 320 330                                                                                                                                    |    |    |    |    |
| DOR-1 | <u>RMVLVVV</u> <u>GAFVV</u> <u>CWAPIH</u> <u>FVIVWTLDINRRDPLVVAALHLCIALGYANSSLNPVLYAELDENFKRCFR</u>                                                            |    |    |    |    |
| rMORa | 280 290 300 310 320 330 340<br><u>RMVLVVV</u> <u>avFivCw</u> <u>tPIH</u> <u>iV</u> <u>ikaLitI-pettfar</u> <u>vswHfcialgytNs</u> <u>cLNPVLYAELDENFKRCFR</u> >   |    |    |    |    |
| rKORa | 280 290 300 310 320 330 340<br><u>k1VLVVV</u> <u>avFiiCw</u> <u>tPIH</u> <u>iFil</u> <u>VeaLgstshsta-al</u> <u>ssvvfcialgytN</u> <u>SSLNPVLYAELDENFKRCFR</u> > |    |    |    |    |
|       | 340 350 360 370                                                                                                                                                |    |    |    |    |
| DOR-1 | <u>QLCRTPCGRQEPGSLRRPQATTRERVTACTPSDGP</u> <u>GGGAAA</u>                                                                                                       |    |    |    |    |
| rMORa | 350 360 370 380<br><u>efCiptsstiEggmstRvRQ-n</u> <u>TR</u> <u>EhpstancvDrtnhglenleae</u> <u>caplp</u>                                                          |    |    |    |    |
| rKORa | 350 360<br><u>dfCfpikmRmErqStnRvRn-Tvgdpasmr</u> <u>rdvvgmnkpv</u> >                                                                                           |    |    |    |    |

Identical amino acids between DOR-1 and mu and kappa receptors in upper case  
Predicted transmembrane domains are underlined

**Figure 10**

Best Available Copy  
 hORL-1 Duano Sequencer  
 Thursday, March 9, 1995 4:06 PM

08/403260

Sequence Range: 1 to 1805

START CODON

↓

\* \* \* \* \*

GGC AGT GGC ATG GAG CCC CTC TTC CCC GCG CCG TTC TGG GAG GTT ATC TAC GGC

54

\* \* \* \* \*

AGC CAC CTT CAG GGC AAC CTG TCC CTC CTG AGC CCC AAC CAC AGT CTG CTG CCC

108

\* \* \* \* \*

CCG CAT CTG CTG CTC AAT GCC AGC CAC GGC GCC TTC CTG CCC CTC GGG CTC AAG

162

\* \* \* \* \*

GTC ACC ATC GTG GGG CTC TAC CTG GCC GTG TGT GTC GGA GGG CTC CTG GGG AAC

216

\* \* \* \* \*

TGC CTT GTC ATG TAC GTC ATC CTC AGG CAC ACC AAA ATG AAG ACA GCC ACC AAT

270

\* \* \* \* \*

ATT TAC ATC TTT AAC CTG GCC CTG GCC GAC ACT CTG GTC CTG CTG ACG CTG CCC

324

\* \* \* \* \*

TTC CAG GGC ACG GAC ATC CTC CTG GGC TTC TGG CCG TTT GGG AAT GCG CTG TGC

378

\* \* \* \* \*

AAG ACA GTC ATT GCC ATT GAC TAC TAC AAC ATG TTC ACC AGC ACC TTC ACC CTA

432

\* \* \* \* \*

ACT GCC ATG AGT GTG GAT CGC TAT GTA GCC ATC TGC GAC CCC ATC CGT GCC CTC

486

\* \* \* \* \*

GAC GTC CGC ACG TCC AGC AAA GCC CAG GCT GTC AAT GTG GCC ATC TGG GCC CTG

540

\* \* \* \* \*

GCC TCT GTT GTC GGT GTT CCC GTT GCC ATC ATG GGC TCG GCA CAG GTC GAG GAT

594

\* \* \* \* \*

GAA GAG ATC GAG TGC CTG GTG GAG ATC CCT ACC CCT CAG GAT TAC TGG GGC CCG

648

\* \* \* \* \*

GTC TTT GCC ATC TGC ATC TTC CTC TTC TCC TTC ATC GTC CCC GTG CTC GTC ATC

702

\* \* \* \* \*

TCT GTC TGC TAC AGC CTC ATG ATC CGG CGG CTC CGT GGA GTC CGC CTG CTC TCG

756

\* \* \* \* \*

GGC TCC CGA GAG AAG GAC CGG AAC CTG CGG CGC ATC ACT CGG CTG GTG CTG GTG

810

Fig 11

hORL-1 Duano Sequence

Thursday, March 9, 1995 4:06 PM

08/403260

864

GTA GTG GCT GTG TTC GTG GCC TGC TGG ACG CCT GTC CAG GTC TTC GTG CTG GCC

918

CAA GGG CTG GGG GTT CAG CCG AGC AGC GAG ACT GCC GTG GCC ATT CTG CGC TTC

972

TGC ACG GCC CTG GCC TAC GTC AAC AGC TGC CTC AAC CCC ATC CTC TAC GCC TTC

1026

CTG GAT GAG AAC TTC AAG GCC TGC TTC CGC AAG TTC TGC TGT GCA TCT GCC CTG

1080

CGC CGG GAC GTG CAG GTG TCT GAC CGC GTG CGC AGC ATT GCC AAG GAC GTG GCC

1134

CTG GCC TGC AAG ACC TCT GAG ACG GTA CCG CGG CCC GCA [TGA] CTA GGC GTG GAC

STOP CODON 1186

CTG CCC ATG GTG CCT GTC AGC CCG CAG AGC CCA TCT ACG CCC AAC ACA GAG CTC

1242

ACA CAG GTC ACT GCT CTC TAG GCG GAC ACA CCC TGG GCC CTG AGC ATC CAG AGC

1296

CTG GGA TGG GCT TTT CCC TGT GGG CCA GGG ATG CTC GGT CCC AGA GGA GGA CCT

1350

AGT GAC ATC ATG GGA CAG GTC AAA GCA TTA GGG CCA CCT CCA TGG CCC CAG ACA

1404

GAC TAA AGC TGC CCT CCT GGT GCA GGG CCG AGG GGA GAC AAG GAC CTA CCT GGA

1458

AGC AGC TGA CAT GCT GGT GGA CGG CCG TTA CTG GAG CCC GTG CCC CTC CCT CCC

1512

CGT GCT TCA TGT GAC TCT TGG CCT CTC TGC TGC TGC GTT GGC AGA ACC CTG GGT

1566

GGG CAG GCA CCC GGA GGA GCA GCA GCT GTG TCA TCC TGT GCC CCC CAT GTG

1620

CTG TGT GCT GTT TGC ATG GCA GGG CTC CAG CTG CCT TCA GCC CTG TGA CGT CTC

1674

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hORL-1 Duano Sequence

Thursday, March 9, 1996 4:06 PM

Page 3

08/403260

CTC AGG GCA GCT GGA CAG GCT TGG CAC GGC CCG GGA AGT GCA GCA GGC AGC TTT

1726

\* \* \* \* \* TCT TTG GGG TGG GAC TTG CCC TGA GCT TGG AGC TGC GAC CTG GAG GAC TTG CCT

1782

\* \* \* \* \* GTT CCG ACT CCA CCT GTG CAG CCG GGG CCA CCC CAG GAG AAA GTG TCC AGG TGG

\* \* \* \* \* GGG CTG GCA GTC CCT GGC TGC AG

|       |                                                                                                                                                                                                                            |     |     |     |     |     |     |
|-------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|-----|-----|-----|-----|-----|
|       | 10                                                                                                                                                                                                                         | 20  | 30  | 40  | 50  | 60  |     |
| hMOR  | MDSSAAPTYAS <del>Y</del> CTDALAYSSCSPAPSPGSW <del>V</del> LSHLDG <del>X</del> LSDPCGP <del>Y</del> RTNLGGRDSLCPPTGSP<br>↑g                                                                                                 |     |     |     |     |     |     |
| hDOR  | mePAPSaGaelq-pplf <del>a</del> <del>Y</del> asDaypsacpsaGa <del>X</del> aSgpParsas                                                                                                                                         |     |     |     |     |     |     |
| mKOR  | mespiqifrgdpgptcspSaC-llP <del>Y</del> ssWfp-nwaesds <del>Y</del> gsvGsedqqLes-ahi-sP-aiP<br>↑ev ↑f                                                                                                                        |     |     |     |     |     |     |
| ORL1  | meplfPaP-fWiygSHLqG <del>Y</del> LSll-sP <del>Y</del> hsllppphill <del>Y</del> ashGal                                                                                                                                      |     |     |     |     |     |     |
| ORL2  | meeggd <del>f</del> dnhygad <del>Y</del> qSeCey <del>T</del> dwk                                                                                                                                                           |     |     |     |     |     |     |
|       | 70                                                                                                                                                                                                                         | 80  | 90  | 100 | 110 | 120 | 130 |
| hMOR  | SMITAITMALYSIVCVGFLGNFLVMVVIVRYT <del>K</del> MKTATNIYIFN <del>L</del> ALADALATSTLPFQS <del>V</del> NY                                                                                                                     |     |     |     |     |     |     |
| hDOR  | SlalAiaItALYSdVCaVGL1GNvLVMfgIVRYTKMKTATNIYIFN <del>L</del> ALADALATSTLPFQS <del>a</del> kY                                                                                                                                |     |     |     |     |     |     |
| mKOR  | -VI-IT--AvYsW <del>F</del> VVGVLGVGnsLVMFV <del>i</del> RYTKMKTATNIYIFN <del>L</del> ALADALvTt <del>T</del> LPFQS <del>a</del> vY                                                                                          |     |     |     |     |     |     |
| ORL1  | plglkvTIvgLYlaVCvgGLIGNcLVMYVILRhtKMKTATNIYIFN <del>L</del> ALADL <del>v</del> l <del>T</del> LPFQ <del>t</del> di                                                                                                         |     |     |     |     |     |     |
| ORL2  | S-sgAl-IpAiYmlVf <del>l</del> GttGNglVlwtfvR <del>s</del> rkrssadIfIasLA <del>v</del> ADltfvvTLPlaty <del>y</del>                                                                                                          |     |     |     |     |     |     |
|       | 140                                                                                                                                                                                                                        | 150 | 160 | 170 | 180 | 190 | 200 |
| hMOR  | LMGTWPFGTILCKIVISIDYYNMFTSIFTLCTMSVDRYIAVCHPV <del>K</del> ALDFR <del>I</del> PRNAKIINVCNWI                                                                                                                                |     |     |     |     |     |     |
| hDOR  | LMetWPFGelLCKaV1S1DYYNMFTSIFTLtmMSVDRYIAVCHPV <del>K</del> ALDFR <del>P</del> akAK1INiC1W                                                                                                                                  |     |     |     |     |     |     |
| mKOR  | LMnsWPFGdvlCKIVISIDYYNMFTSIFTLtmMSVDRYIAVCHPV <del>K</del> ALDFR <del>P</del> 1KAK1INiC1W                                                                                                                                  |     |     |     |     |     |     |
| ORL1  | L1GWPFGn <del>a</del> lCK <del>e</del> V <del>i</del> aIDYYNMFTSIFTLtmMSVDRYIAVCHP <del>r</del> 1ALD <del>V</del> RT <del>s</del> skAqavN <del>v</del> iMa                                                                 |     |     |     |     |     |     |
| ORL2  | rdy <del>d</del> WPFGTffCK1ssyli <del>f</del> vN <del>y</del> aSvFc <del>t</del> tg <del>l</del> sfDRY1aivrP <del>v</del> anariRlr <del>v</del> sgavatav <del>l</del> W                                                    |     |     |     |     |     |     |
|       | 210                                                                                                                                                                                                                        | 220 | 230 | 240 | 250 | 260 |     |
| hMOR  | LSSAIGLPVHMFMATTKYRQGSIDCTLTFSHPTWWENLVKICVFIFAVPVL <del>I</del> ITV <del>C</del> YGLMILR                                                                                                                                  |     |     |     |     |     |     |
| hDOR  | LaSgvGvPiMvMAvTrpRdgavvCmlqFpsPsWY <del>W</del> dtvtKICVF1FAFv <del>v</del> Pi <del>I</del> ITV <del>C</del> YGLMILR<br>↑dv      Tys                                                                                       |     |     |     |     |     |     |
| mKOR  | LaSsvGisaiVlggTKvRedvIe <del>s</del> LqFpddeW-Wd1fmKICVFvFAFv <del>i</del> PVLI <del>I</del> IVCYtLMI <del>R</del>                                                                                                         |     |     |     |     |     |     |
| hORL1 | LaSvvGvP <del>v</del> aiMgsaqvedeeIe <del>c</del> lveiptPqdY <del>W</del> gpvfa <del>i</del> CiFlFsFv <del>v</del> PV <del>l</del> V <del>i</del> sVC <del>y</del> sLM <del>i</del> <del>R</del><br>↑r      ↑k      ↑mvatv |     |     |     |     |     |     |
| hORL2 | LaallamP <del>V</del> MvltTgdle <del>n</del> ttvqCymdySsseWa <del>W</del> EvgIgvsssttvgFv <del>v</del> PftImltCY-ffIaq                                                                                                     |     |     |     |     |     |     |
|       | 270                                                                                                                                                                                                                        | 280 | 290 | 300 | 310 | 320 | 330 |
| hMOR  | LKS <del>V</del> RMLSGSKEKDRNLRR <del>I</del> IRMV <del>L</del> VVVAVFIVCWTPIHIV <del>I</del> Y <del>I</del> KALVT <del>I</del> PETTFQTV <del>S</del> WHFCIA<br>↑d                                                         |     |     |     |     |     |     |
| hDOR  | L <del>r</del> S <del>V</del> R <del>l</del> LSGSKEKDR <del>s</del> LRR <del>I</del> IRMV <del>L</del> VVVgaFwC <del>w</del> aPIHIFV <del>i</del> w <del>t</del> L <del>v</del> dIrrdpl <del>v</del> aa <del>h</del> 1CIA  |     |     |     |     |     |     |
| mKOR  | LKS <del>V</del> R <del>l</del> LSGS <del>r</del> EKDRNLRR <del>I</del> IK1LVVVAVFI <del>i</del> CWTPIHIFil <del>v</del> eAl <del>g</del> stshsTa <del>l</del> sSyyFCIA                                                    |     |     |     |     |     |     |
| ORL1  | Lrg <del>V</del> R <del>l</del> LSGS <del>r</del> EKDRNLRR <del>I</del> IR1LVVVAVFvgCWT <del>P</del> qv <del>f</del> Vla <del>q</del> gLgvqP <del>s</del> setavailrFC <del>A</del><br>↑lvkt      ↑f                        |     |     |     |     |     |     |
| ORL2  | tiaghfrkeriEglRkrR <del>l</del> 1sii <del>v</del> lvvt <del>f</del> alC <del>w</del> PyH1Ymlgs <del>l</del> lhwp <del>c</del> dd <del>l</del> Flmnif <del>p</del> yCtc                                                     |     |     |     |     |     |     |
|       | 340                                                                                                                                                                                                                        | 350 | 360 | 370 | 380 | 390 |     |
| hMOR  | LGYN <del>S</del> CLNPVLYAFLDENFKRCFR <del>E</del> FC <del>F</del> CIPTSSNIEQQN <del>S</del> TRIRQ <del>N</del> IRDHP <del>S</del> ANTV <del>D</del> RTNHQ <del>L</del>                                                    |     |     |     |     |     |     |
| hDOR  | LGY <del>a</del> NS <del>S</del> CLNPVLYAFLDENFKRCFR <del>q</del> lCrkpcgrpdpsfsRaRe <del>l</del> ar <del>er</del> vTA <del>c</del> tps <del>d</del> gpggg <del>a</del> >                                                  |     |     |     |     |     |     |
| mKOR  | LGYT <del>N</del> SS <del>S</del> CLNPVLYAFLDENFKRCFR <del>d</del> FC <del>P</del> 1kmrm <del>Er</del> Q <del>s</del> <del>t</del> nRvR-NT <del>v</del> qdPasmrdVggmnkp <del>v</del>                                       |     |     |     |     |     |     |
| ORL1  | LGY <del>w</del> NS <del>C</del> LN <del>P</del> LYAFLDENFK <del>a</del> CFRK <del>C</del> casalrrdvQ <del>s</del> dRvR <del>s</del> ia <del>k</del> DvalackTsetvprpa<br>↑q                                                |     |     |     |     |     |     |
| ORL2  | isYvNS <del>C</del> LN <del>P</del> FLYAFFDprFr <del>a</del> tsmlCcgqSrcagtshS <del>s</del> geksasyssghs <del>q</del> gpgpnmgkg                                                                                            |     |     |     |     |     |     |
|       | 400.                                                                                                                                                                                                                       |     |     |     |     |     |     |
| hMOR  | NLEAETAPLP                                                                                                                                                                                                                 |     |     |     |     |     |     |
| hDOR  | aa                                                                                                                                                                                                                         |     |     |     |     |     |     |
| ORL2  | eqmh <del>e</del> ksipysqetl <del>v</del> vd                                                                                                                                                                               |     |     |     |     |     |     |

Fig 1. COMPARISON OF ORL1 & ORL2 PROTEIN SEQUENCES WITH  $\mu$ ,  $\delta$  &  $\kappa$  RECEPTORS  
 Regions overscored with ~~.....~~ represent predicted transmembrane domains. The symbol ~~Y~~ represents extracellular Asn residues that are consensus sites for N-linked glycosylation. Consensus PKA/PKC sites are underlined. The Genbank references are: for hMOR (Human mu receptor), Wang et al., Accession# L25119; for hDOR (human delta opioid receptor) Simonin et al., Accession# U10504; and for mKOR (murine kappa opioid receptor), Yasuda et al., Accession# L11065.